

Resource Summary Report

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FASTX-Toolkit

RRID:SCR_005534

Type: Tool

Proper Citation

FASTX-Toolkit (RRID:SCR_005534)

Resource Information

URL: http://hannonlab.cshl.edu/fastx_toolkit/

Proper Citation: FASTX-Toolkit (RRID:SCR_005534)

Description: Software tool as collection of command line tools for Short-Reads FASTA/FASTQ files preprocessing.

Synonyms: FASTQ/A short-reads pre-processing tools

Resource Type: software toolkit, software resource, software application, data processing software

Keywords: Short reads, FASTA file, FASTQ file, preprocessing, command line tools, bio.tools

Resource Name: FASTX-Toolkit

Resource ID: SCR_005534

Alternate IDs: SCR_019035, SCR_015042, biotools:fastx-toolkit, OMICS_01045

Alternate URLs: https://github.com/agordon/fastx_toolkit, <https://bio.tools/fastx-toolkit>

License: Affero GPL (AGPL)

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260731T042712+0000

Ratings and Alerts

No rating or validation information has been found for FASTX-Toolkit.

No alerts have been found for FASTX-Toolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2600 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Hiltunen J, et al. (2025) Androgen receptor-mediated assisted loading of the glucocorticoid receptor modulates transcriptional responses in prostate cancer cells. *Genome research*, 35(8), 1717.

Feckler A, et al. (2025) Antimicrobials Shape the Gut Microbiome Structure and Digestive Profile of Invertebrates. *Environmental science & technology*, 59(37), 19667.

Guajardo-Leiva S, et al. (2025) From sewage to genomes: Expanding our understanding of the urban and semi-urban wastewater RNA virome. *Environmental research*, 276, 121509.

Tatarakis A, et al. (2025) Requirements for establishment and epigenetic stability of mammalian heterochromatin. *Molecular cell*, 85(18), 3388.

Tonnelé H, et al. (2025) Genetic architecture and mechanisms of host-microbiome interactions from a multi-cohort analysis of outbred laboratory rats. *Nature communications*, 16(1), 10126.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1), 21.

Chen S, et al. (2025) Nuclear Argonaute protein NRDE-3 switches small RNA partners during embryogenesis to mediate temporal-specific gene regulatory activity. *eLife*, 13.

Ignatov D, et al. (2025) RNA-binding protein YebC enhances translation of proline-rich amino acid stretches in bacteria. *Nature communications*, 16(1), 6262.

Dong J, et al. (2025) ZNF143 binds DNA and stimulates transcription initiation to activate and repress direct target genes. *Nucleic acids research*, 53(2).

Wang H, et al. (2025) Comparative transcriptomes reveal insights into different host responses associated with *Fusarium* head blight resistance in wheat. *BMC plant biology*, 25(1), 509.

Pradel N, et al. (2025) Complete genome sequence of Nitratireductor aquimarinus strain MNA2.1 isolated from sediments of the Berre lagoon, France. *Microbiology resource announcements*, 14(10), e0025925.

Duffié R, et al. (2025) Mex3a-dependent post-transcriptional silencing ensures olfactory receptor diversity and axon guidance specificity. *Cell reports*, 44(8), 115979.

Qi Y-H, et al. (2025) Diversity and evolutionary history of RNA viruses among different horseshoe crab species. *Journal of virology*, 99(7), e0016425.

Sullivan SA, et al. (2025) Comparative genomics of the parasite *Trichomonas vaginalis* reveals genes involved in spillover from birds to humans. *Nature communications*, 16(1), 6487.

Raab M, et al. (2025) Two decades long-term field trial data on fertilization, tillage, and crop rotation focusing on soil microbes. *Scientific data*, 12(1), 986.

Sharma A, et al. (2025) Group A Streptococcal asparagine metabolism regulates bacterial virulence. *EMBO reports*, 26(10), 2767.

Liu D, et al. (2025) Proto-oncogene DEK binds to pre-mRNAs and regulates the alternative splicing of Hippo signaling genes in HeLa cells. *Molecular genetics and genomics* : MGG, 300(1), 31.

Li S, et al. (2025) Integrative characterization of MYC RNA-binding function. *Cell genomics*, 5(7), 100878.

Nariman N, et al. (2025) The Microbiome of an Invasive Spider: Reduced Bacterial Richness, but no Indication of Microbial-Mediated Dispersal Behaviour. *Microbial ecology*, 88(1), 70.